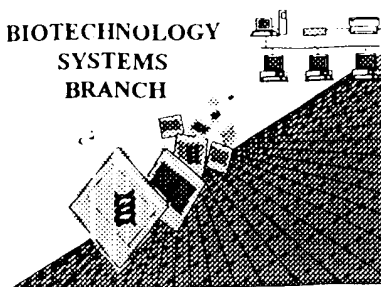


RAW SEQUENCE LISTING **ERROR REPORT**

BIOTECHNOLOGY
SYSTEMS
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/727,855A

Source: 1645

Date Processed by STIC: 6/7/2001

RECEIVED

JUN 27 2001

TECH CENTER 1600/2000

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

JUN 27 1998

Raw Sequence Listing Error Summary

TECH CENTER 1001 2800

ERROR DETECTEDSUGGESTED CORRECTIONSERIAL NUMBER: 09/722,855A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line **not** exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.
- 4 Non-ASCII The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. Please ensure your **subsequent submission is saved in ASCII text**.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for **each** skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for **each** skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000
- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.
 In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.
- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is **MANDATORY** if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

1645

RAW SEQUENCE LISTING

DATE: 06/07/2001

PATENT APPLICATION: US/09/727,855A

TIME: 14:25:41

Input Set : A:\SeqListing.txt

Output Set: C:\CRF3\06072001\I727855A.raw

f.b

3 <110> APPLICANT: F. HOFFMANN-LA ROCHE AG
 5 <120> TITLE OF INVENTION: PROCESS FOR THE MANUFACTURE OF CAROTENOIDS AND
 6 BIOLOGICALLY USEFUL MATERIALS THEREOF
 8 <130> FILE REFERENCE: SOD
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/727,855A
 C--> 11 <141> CURRENT FILING DATE: 2000-12-01
 13 <150> PRIOR APPLICATION NUMBER: EP99123821.3
 14 <151> PRIOR FILING DATE: 1999-12-01
 16 <160> NUMBER OF SEQ ID NOS: 17
 18 <170> SOFTWARE: PatentIn Ver. 2.0
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 21 <211> LENGTH: 3632
 22 <212> TYPE: DNA
 23 <213> ORGANISM: Phaffia rhodozyma
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 26 <221> NAME/KEY: 5'UTR
 27 <222> LOCATION: (922)..(923)
 28 <223> OTHER INFORMATION: EXPERIMENTAL
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 64 <222> LOCATION: (1921)..(1982)
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RAW SEQUENCE LISTING

DATE: 06/07/2001

PATENT APPLICATION: US/09/727,855A

TIME: 14:25:41

Input Set : A:\SeqListing.txt

Output Set: C:\CRF3\06072001\I727855A.raw

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82 <220> FEATURE:
83 <221> NAME/KEY: intron
84 <222> LOCATION: (2273)..(2390)
86 <220> FEATURE:
87 <221> NAME/KEY: exon
88 <222> LOCATION: (2391)..(2507)
90 <220> FEATURE:
91 <221> NAME/KEY: polyA_site
92 <222> LOCATION: (2663)..(2664)
93 <223> OTHER INFORMATION: EXPERIMENTAL
95 <400> SEQUENCE: 1
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100 agtatgacga tggtagaggt gaaggaggga accacaggtt gaccagtctc aaagagtgtc 180
102 gatgtgcgcg aggtattgtc attaaatggt gttgtatatg ctagagccaa gagaagacat 240
104 ttggtttttg ttttggtttt gcatttgatg agatgtgtca cgattgaaga cgggaggagg 300
106 ctcaactaac caagaagcca ggatcaggag gaatgcctcc cctttttcat caagatcttt 360
108 ctacacatga acatttgaca ttctctttag tatccttcta tctttttctt ccaactttct 420
110 ccattgtatc gactttgtct gacttgcctt tcttatctct gacgagagat gggcattcca 480
112 atatcgaaag agcgacacaa gaccttggag tttgggtaac agatgaagag gggccgaggt 540
114 ggatggggct gtaggaagta gctgatcgat gagttcctgg atgatgatag gcgaaggaaac 600
116 agacatagga tctctgtctc gtctggaat tactgagctt tgtatccagc gtgtttctgt 660
118 ctogaagaag ccttcaagat cgatgtaaga taagacaggc aatgaggacg gacgaacgaa 720
120 cgaacgaaaa gaacagaaga gctggtaagt cagtcagtca gtcagtcagt caatcaaaaca 780
122 ctggtgtcta gggttataga tcgacgcgac gcgacgcgtt tgagacgca tatgcttacg 840
124 taatacctgg cgtcatcccc ccagccgagg caagagccga gccgctcgtg aacgacaaaa 900
126 ttcaaaaagg tttctccatc ttaagctcat tctcatctaa ccgactcacc tcgttcccat 960
128 cattcccatc attctacccc catcc atg tct gtt cga gca tcc ctg tct tcc 1012
130 gtg tct aga cag act ttc gtc gct cct gct gct ttc cag atc agg gca 1060
132 aag cat acc ctg cct gag ctt cct tac gct tac gat gtaagacttt 1106
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136 tcgtcttttc tgtcctgtct tttgttgttg atattcagct cgatagacta acccatctca 1226
138 tctcttgga cttctttttac tggaaaagta tcttgcctt ggtttttctt ggctttgggt 1286
140 gaaaattcct ctcaactcag gcc ctg gag ccc tcc atc tcc aag gag atc atg 1339
142 acc ctt cac cac acc aag cac cat cag act tat gtt aac ggc ctg aac 1387
144 gct gcc gag gag agc tac tgg gcc gct gtg ggc aag gag gat gtg ctt 1435
146 acc cag gtt aag ctt cag tct gtaagctga cgttttttt atcgaccgga 1486
148 acgcctgggt agggaggaga tgaagtttga tgagcgtca tcgtctagca cgttgaccgg 1546
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RAW SEQUENCE LISTING

DATE: 06/07/2001

PATENT APPLICATION: US/09/727,855A

TIME: 14:25:41

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Output Set: C:\CRF3\06072001\I727855A.raw

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154 gttttctggg atctatctca tcttgattt ggcctgatga aacag ac tct ctg ttc 1705
156 tgg aag aac ttg gct ccc tat gga tcc gag gag gct acc ctg tct gaa 1753
158 gga cct ctg aag aag gct atc gag gaa tct ttt ggt tct ttc gag g 1799
160 gtcctgcat ctatcttctt attcagttgt gtttggttcc ggtatactca tctgtttgt 1859
162 tttccacaaa aataaaaaata aaaattttgt cctctcggg ggttcgactg caagttcata 1919
164 g cc ttc aag aag aag ttc aac gct gac acc gct gct gtc caa gga tcc 1967
166 gga tgg ggc tgg ctt gtatgtatca tctctttcc atctcaaaact cttctcagag 2022
168 tttttttctt tgagacttca aactgactat acatgtttct acaacaaaca acag ggc 2079
170 ttg aac ccg ctt act aag aag ctg gaa gtc acc acg acc gcc aac cag 2127
172 gac cct ctg ctt a gtaagttgtt tctacatgat tttctatctc aacgcatct 2180
174 gcctgattcg tcaactgattc actggattct cttgtttcgt tttctcggg atgatttcat 2240
176 aaacag ct cac att cct atc atc gga gtt gac gtgcgtatct ttctgaata 2292
178 gtgtagcgt ctgactctgt tttattgact gacgtgttg tctgttcaa atcattaaaa 2352
180 aaatgaaaa caataatcg attgacggac gaaaacag atc tgg gag cac gct ttc 2408
182 tac ctt cag tac aag aac gtc aag cct gac tat ctg gct gct gtt tgg 2456
184 tcc gtt atc aac tac aag gag gca gag gcc cga ttg cag gct gct ctg 2504
186 taa gcgggacgaa aagtaacgac atatgaaggg aggatcaaat atcgtttctt 2557
188 cataaacaac tttcgaggca gatgggagag tacgtacaag agaggtttgt atggagaatt 2617
190 gagtttgttg aoggttagca ggttatgata tatgtagcta tagtctagtc taaatctgaa 2677
192 agaagagaac aagatggttt gtccgaagag attgagagat caagcccggt catctgagt 2737
194 cgaacaaaaca tgccttggtc tgcacacagt ttctagcaca ttatgaacct gtccatgtgt 2797
196 aaattgggaa atgagccaga aaggtttatt atctaattca ttgattcatg cgaactatgga 2857
198 tacatatggg atttccagaa caaacagatg caacaaagca cggcattttc caaagatoga 2917
200 gtctctccac aagtatggcg caaggtttgt tgttaagaga tataaaaagca gacgacaaaa 2977
202 caaatctgtt atcgacctg tgcaccaaca ccgtgacctt ttgacgagtt ggtagagttg 3037
204 tagttgttgc tgttcaaaag agctccagac tggacgcttc caagcttcaa caactctctg 3097
206 ggcgctctgc tgttcgggaa aagaaaaggc aaaaagggaac agagcgataa gcataatgtga 3157
208 ttctctactt cttataggct cttagctcaa gtcaactcac atgtctttgg cggtaacgaa 3217
210 gacgttctca agctgctgct tggaaagctt tccgagcttg ccagtaggtc cctgggttga 3277
212 gaagaagatg togaaggcta agggcgatga aaagcatgaa gatattagct atcggcgoga 3337
214 taaaagtgtg acgagatgaa aatggagaaa agatgattcg caccatcgac gacctcgacc 3397
216 aaaggaatgg aggtgtcacc ggcttccac ttctgtact cctcaacgtt gacgaagatg 3457
218 acgaagcagt cgttgccctt agctcgggc tcttagatgc tgatgaaaca caataggtag 3517
220 taggagagga gaaagagaag atgatgatg gtcaggatgc ttgttccact gtagatggag 3577
222 gaagaagata tgcgaagcaa gacatacact ttggaagag cttgaacctat tgtag 3632

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225 <210> SEQ ID NO: 2

226 <211> LENGTH: 3375

227 <212> TYPE: DNA

228 <213> ORGANISM: Phaffia rhodozyma

230 <220> FEATURE:

231 <221> NAME/KEY: 5'UTR

232 <222> LOCATION: (974)..(975)

233 <223> OTHER INFORMATION: EXPERIMENTAL

235 <230> FEATURE:

236 <231> NAME/KEY: exon

237 <232> LOCATION: (1040)..(1063)

239 <220> FEATURE:

240 <221> NAME/KEY: intron

RAW SEQUENCE LISTING

DATE: 06/07/2001

PATENT APPLICATION: US/09/727,855A

TIME: 14:25:41

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Output Set: C:\CRF3\06072001\I727855A.raw

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268 <221> NAME/KEY: exon
269 <222> LOCATION: (1675)..(1826)
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300 <221> NAME/KEY: exon
301 <222> LOCATION: (2239)..(2293)
303 <220> FEATURE:
304 <221> NAME/KEY: intron
305 <222> LOCATION: (2294)..(2376)

RAW SEQUENCE LISTING

DATE: 06/07/2001

PATENT APPLICATION: US/09/727,855A

TIME: 14:25:41

Input Set : A:\SeqListing.txt

Output Set: C:\CRF3\06072001\I727855A.raw

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307 <220> FEATURE:
308 <221> NAME/KEY: exon
309 <222> LOCATION: (2377)..(2426)
311 <220> FEATURE:
312 <221> NAME/KEY: intron
313 <222> LOCATION: (2427)..(2524)
315 <220> FEATURE:
316 <221> NAME/KEY: exon
317 <222> LOCATION: (2525)..(2542)
319 <220> FEATURE:
320 <221> NAME/KEY: polyA_site
321 <222> LOCATION: (2667)..(2668)
322 <223> OTHER INFORMATION: EXPERIMENTAL
324 <400> SEQUENCE: 2
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327 ctatacgaag ggtagcgcag agcaaagctg acagtattaa gcaagacaag agcttctttc 120
329 tggttgacaga tgaaaggacg aactatgaag ctgtccatgc tccccaaacc gattgacaca 180
331 cgcgcgtcag gcaacgcaga atttctcact gcttcgacgt cacaccaaca tcgatccctc 240
333 atacctaaaa gcagatcgag acacattggt ggtcgccatg ttggatggat gtacatcaaa 300
335 cccacagcat atatactca catgtgagaa ctccgtagcc tctaccttct tgtctctcaa 360
337 tctgaatgtc tctgttgagag gtggaatgaa tgtttacagt ttgagaagac gaaagaaaga 420
339 aagagaagag aagagaggaa tacgtacgac gaagttatca tcgtatggga actttttctaa 480
341 aaaactgcct atagtagaga cgatctcttg aggaaagctc tgtagtatga tagtgaagag 540
343 cgagcaagtc tgggcaagtg catccttcgt ctacaagaaa gagaccagga aatgaaggag 600
345 agaagagtaa gcaggtacct accgatattg gatcgttctc tctaccacgc gatgccttca 660
347 ccaacgcgttc tatctcttct tgggatggca gatacatact taacgagagc aatctgatgt 720
349 ataccgaact tgaacggaa tgatcccaga atcctcttga acccttgaac ccttgaaccc 780
351 tggaaccaag taccaccca gcaaacgcc gatacgggcc acaccacaga accacacgcc 840
353 ctgcctatta aaggtgggac gcgcgatgc tggttacgtt cggcccaatc cggaagttac 900
355 cggtttggac gtgcctgtaa ccatgccttg acggtatttc gccttcagct aactccatct 960
357 catctttttc ctttactacc acaaccacc cttgaacctt cttccccggc ttttttacta 1020
359 tatccatcta tcaatcata atg gct cct tac act ctt ccc gac gtaagcttaa 1073
361 agtttgagct gtgtgtgctt atctcaatct tggagttgaa ctaccggtt tttgtttttg 1133
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369 gttgttccgg ttgcacacga tagctaactg tctctcgttc ctcaatatga acatgcag 1358
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373 gtaagtaate taaaggtcat ctccgtctac atggccggat caacttctc atagatcttc 1462
375 cttctgttcg gcgtacgta g acc aac ctg aac gcc gct atc cag gct ttc 1513
377 tcc cag acc aat gac atc aag gcc cag atc gct ctt cag agc gct ctg 1561
379 aag ttc aac gga gga gga cac atc aac c gtacgatcat tctcctctt 1609
381 ctggtttatc atatgtgttg cttgtcacta acacgcagtc aaccccgga tatctcacc 1669
383 tgtag ac tcc ctg ttc tgg aag aac atg gct cct gcc gac tct gct gat 1718
385 gcc aag ctg acc gag gga tgg ctg aag act gcc atc gac aag gac ttt 1766
387 gga tcc ttc gag gag ttc aag aag aag ttc aac act gct act ctg ggt 1814
389 gtc cag gga tct gtcagtatct cgtttgcttc gacatactct cagctttcct 1866
391 tccgtaaaact gacgaatagt ttttcggaca tgtacttgta g gga tgg gga tgg ctg 1922
393 gtgcgtttga cctttttcca ctttgaacat tagcgatagt gatacctaac aactgtgaat 1982

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<210> 10
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Sod1(sense
 primer for cloning of SOD genes)

<400> 10
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→ see item 9 on Error Summary Sheet

23

<210> 11
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Sod4 (antisense
 primer for cloning of SOD genes)

<400> 11
 gccanccng anccytgnac ncc

↓
 item 9

23

The types of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/727,855A

DATE: 06/07/2001

TIME: 14:25:42

Input Set : A:\SeqListing.txt

Output Set: C:\CRF3\06072001\I727855A.raw

L:10 M:270 C: Current Application Number differs, Replaced Application Number
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:881 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:10
L:881 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:10
L:881 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:894 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:11
L:894 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:11
L:894 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:963 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:16
L:963 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:16
L:963 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:976 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:17
L:976 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:17
L:976 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17